RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/529,278_

Source: _PCT/10_

Date Processed by STIC: _12/20/05_

ENTERED

PCT

RAW SEQUENCE LISTING   DATE: 12/20/2005
PATENT APPLICATION: US/10/529,278   TIME: 10:29:11

        Input Set : A:\11582-010-999 Seqlist.txt
        Output Set: N:\CRF4\12202005\J529278.raw

  4 <110> APPLICANT: Inbe, Hisayo
  5   Encinas, Jeffrey
  7 <120> TITLE OF INVENTION: Regulation of Human P2Y15 G
  8   Protein-Coupled Receptor
 10 <130> FILE REFERENCE: 11582-010-999
 12 <140> CURRENT APPLICATION NUMBER: 10/529,278
 13 <141> CURRENT FILING DATE: 2005-03-25
 15 <150> PRIOR APPLICATION NUMBER: PCT/EP2003/010666
 16 <151> PRIOR FILING DATE: 2003-09-25
 18 <150> PRIOR APPLICATION NUMBER: 60/442,891
 19 <151> PRIOR FILING DATE: 2003-01-28
 21 <150> PRIOR APPLICATION NUMBER: 60/413,840
 22 <151> PRIOR FILING DATE: 2002-09-27
 24 <160> NUMBER OF SEQ ID NOS: 10
 26 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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 30 <212> TYPE: DNA
 31 <213> ORGANISM: Homo Sapiens
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 43 Tyr Ala Ala Ala Phe Gly Asn Cys Thr Asp Glu Asn Ile Pro Leu Lys
 44   20   25   30
 46 atg cac tac ctc cct gtt att tat ggc att atc ttc ctc gtg gga ttt   144
 47 Met His Tyr Leu Pro Val Ile Tyr Gly Ile Ile Phe Leu Val Gly Phe
 48   35   40   45
 50 cca ggc aat gca gta gtg ata tcc act tac att ttc aaa atg aga cct   192
 51 Pro Gly Asn Ala Val Val Ile Ser Thr Tyr Ile Phe Lys Met Arg Pro
 52   50   55   60
 54 tgg aag agc agc acc atc att atg ctg aac ctg gcc tgc aca gat ctg   240
 55 Trp Lys Ser Ser Thr Ile Ile Met Leu Asn Leu Ala Cys Thr Asp Leu
 56 65   70   75   80
 58 ctg tat ctg acc agc ctc ccc ttc ctg att cac tac tat gcc agt ggc   288
 59 Leu Tyr Leu Thr Ser Leu Pro Phe Leu Ile His Tyr Tyr Ala Ser Gly
 60   85   90   95
 62 gaa aac tgg atc ttt gga gat ttc atg tgt aag ttt atc cgc ttc agc   336
 63 Glu Asn Trp Ile Phe Gly Asp Phe Met Cys Lys Phe Ile Arg Phe Ser

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70 atc ttc cgc tac tgt gtg atc att cac cca atg agc tgc ttt tcc att    432
71 Ile Phe Arg Tyr Cys Val Ile Ile His Pro Met Ser Cys Phe Ser Ile
72      130              135              140
74 cac aaa act cga tgt gca gtt gta gcc tgt gct gtg gtg tgg atc att    480
75 His Lys Thr Arg Cys Ala Val Val Ala Cys Ala Val Val Trp Ile Ile
76 145              150              155              160
78 tca ctg gta gct gtc att ccg atg acc ttc ttg atc aca tca acc aac    528
79 Ser Leu Val Ala Val Ile Pro Met Thr Phe Leu Ile Thr Ser Thr Asn
80              165              170              175
82 agg acc aac aga tca gcc tgt ctc gac ctc acc agt tcg gat gaa ctc    576
83 Arg Thr Asn Arg Ser Ala Cys Leu Asp Leu Thr Ser Ser Asp Glu Leu
84            180              185              190
86 aat act att aag tgg tac aac ctg att ttg act gca act act ttc tgc    624
87 Asn Thr Ile Lys Trp Tyr Asn Leu Ile Leu Thr Ala Thr Thr Phe Cys
88            195              200              205
90 ctc ccc ttg gtg ata gtg aca ctt tgc tat acc acg att atc cac act    672
91 Leu Pro Leu Val Ile Val Thr Leu Cys Tyr Thr Thr Ile Ile His Thr
92      210              215              220
94 ctg acc cat gga ctg caa act gac agc tgc ctt aag cag aaa gca cga    720
95 Leu Thr His Gly Leu Gln Thr Asp Ser Cys Leu Lys Gln Lys Ala Arg
96 225              230              235              240
98 agg cta acc att ctg cta ctc ctt gca ttt tac gta tgt ttt tta ccc    768
99 Arg Leu Thr Ile Leu Leu Leu Leu Ala Phe Tyr Val Cys Phe Leu Pro
100              245              250              255
102 ttc cat atc ttg agg gtc att cgg atc gaa tct cgc ctg ctt tca atc    816
103 Phe His Ile Leu Arg Val Ile Arg Ile Glu Ser Arg Leu Leu Ser Ile
104            260              265              270
106 agt tgt tcc att gag aat cag atc cat gaa gct tac atc gtt tct aga    864
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108            275              280              285
110 cca tta gct gct ctg aac acc ttt ggt aac ctg tta cta tat gtg gtg    912
111 Pro Leu Ala Ala Leu Asn Thr Phe Gly Asn Leu Leu Leu Tyr Val Val
112      290              295              300
114 gtc agc gac aac ttt cag cag gct gtc tgc tca aca gtg aga tgc aaa    960
115 Val Ser Asp Asn Phe Gln Gln Ala Val Cys Ser Thr Val Arg Cys Lys
116 305              310              315              320
118 gta agc ggg aac ctt gag caa gca aag aaa att agt tac tca aac aac    1008
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132 <213> ORGANISM: Homo Sapiens
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140         35                  40                  45
141 Pro Gly Asn Ala Val Val Ile Ser Thr Tyr Ile Phe Lys Met Arg Pro
142     50                  55                  60
143 Trp Lys Ser Ser Thr Ile Ile Met Leu Asn Leu Ala Cys Thr Asp Leu
144 65                  70                  75                  80
145 Leu Tyr Leu Thr Ser Leu Pro Phe Leu Ile His Tyr Tyr Ala Ser Gly
146             85                  90                  95
147 Glu Asn Trp Ile Phe Gly Asp Phe Met Cys Lys Phe Ile Arg Phe Ser
148             100                 105                 110
149 Phe His Phe Asn Leu Tyr Ser Ser Ile Leu Phe Leu Thr Cys Phe Ser
150         115                 120                 125
151 Ile Phe Arg Tyr Cys Val Ile Ile His Pro Met Ser Cys Phe Ser Ile
152     130                 135                 140
153 His Lys Thr Arg Cys Ala Val Val Ala Cys Ala Val Val Trp Ile Ile
154 145                 150                 155                 160
155 Ser Leu Val Ala Val Ile Pro Met Thr Phe Leu Ile Thr Ser Thr Asn
156             165                 170                 175
157 Arg Thr Asn Arg Ser Ala Cys Leu Asp Leu Thr Ser Ser Asp Glu Leu
158             180                 185                 190
159 Asn Thr Ile Lys Trp Tyr Asn Leu Ile Leu Thr Ala Thr Thr Phe Cys
160         195                 200                 205
161 Leu Pro Leu Val Ile Val Thr Leu Cys Tyr Thr Thr Ile Ile His Thr
162     210                 215                 220
163 Leu Thr His Gly Leu Gln Thr Asp Ser Cys Leu Lys Gln Lys Ala Arg
164 225                 230                 235                 240
165 Arg Leu Thr Ile Leu Leu Leu Leu Ala Phe Tyr Val Cys Phe Leu Pro
166             245                 250                 255
167 Phe His Ile Leu Arg Val Ile Arg Ile Glu Ser Arg Leu Leu Ser Ile
168         260                 265                 270
169 Ser Cys Ser Ile Glu Asn Gln Ile His Glu Ala Tyr Ile Val Ser Arg
170         275                 280                 285
171 Pro Leu Ala Ala Leu Asn Thr Phe Gly Asn Leu Leu Leu Tyr Val Val
172     290                 295                 300
173 Val Ser Asp Asn Phe Gln Gln Ala Val Cys Ser Thr Val Arg Cys Lys
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182 <212> TYPE: DNA
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195 Tyr Pro Ser Ala Leu Gly Asn Cys Thr Asp Glu Gln Ile Ser Phe Lys
196             20                  25                  30
198 atg cag tac ctt ccc gtc atc tat agc atc atc ttc ctc gtg ggc ttc   144
199 Met Gln Tyr Leu Pro Val Ile Tyr Ser Ile Ile Phe Leu Val Gly Phe
200         35                  40                  45
202 ccg ggg aac aca gtg gcc atc tcc atc tac att ttc aag atg cgg ccg   192
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204     50                  55                  60
206 tgg agg ggc agt aca gtc atc atg ctg aac ctg gcc ttg acg gac ttg   240
207 Trp Arg Gly Ser Thr Val Ile Met Leu Asn Leu Ala Leu Thr Asp Leu
208 65                  70                  75                  80
210 ctg tat ctg acc agc ctc ccg ttc ctc atc cat tac tat gcc agt ggt   288
211 Leu Tyr Leu Thr Ser Leu Pro Phe Leu Ile His Tyr Tyr Ala Ser Gly
212                 85                  90                  95
214 gaa aac tgg atc ttt gga gat ttc atg tgc aag ttc atc cgc ttc ggc   336
215 Glu Asn Trp Ile Phe Gly Asp Phe Met Cys Lys Phe Ile Arg Phe Gly
216             100                 105                 110
218 ttc cac ttc aac ctc tac agc agc att ctc ttc ctc acc tgc ttc agt   384
219 Phe His Phe Asn Leu Tyr Ser Ser Ile Leu Phe Leu Thr Cys Phe Ser
220         115                 120                 125
222 ctc ttc cgt tac gtt gtg atc att cac ccg atg agc tgc ttt tct att   432
223 Leu Phe Arg Tyr Val Val Ile Ile His Pro Met Ser Cys Phe Ser Ile
224     130                 135                 140
226 cag aaa act cgc tgg gca gtg gta gct tgt gcc ggg gtg tgg gtc att   480
227 Gln Lys Thr Arg Trp Ala Val Val Ala Cys Ala Gly Val Trp Val Ile
228 145                 150                 155                 160
230 tct ttg gta gct gtc atg ccc atg act ttc ctg atc aca tca acc acc   528
231 Ser Leu Val Ala Val Met Pro Met Thr Phe Leu Ile Thr Ser Thr Thr
232                 165                 170                 175
234 cgg acc aat agg tct gct tgc ctt gac ctc acc agt tca gat gac ctc   576
235 Arg Thr Asn Arg Ser Ala Cys Leu Asp Leu Thr Ser Ser Asp Asp Leu
236             180                 185                 190
238 act act atc aag tgg tac aat ctc att ttg aca gcc acc act ttc tgc   624
239 Thr Thr Ile Lys Trp Tyr Asn Leu Ile Leu Thr Ala Thr Thr Phe Cys
240         195                 200                 205
242 ctg cca ttg gtg ata gtg aca ctt tgc tac acg aca att atc agt acc   672
243 Leu Pro Leu Val Ile Val Thr Leu Cys Tyr Thr Thr Ile Ile Ser Thr
244     210                 215                 220
246 ctg act cac ggg cct cgg acc cac agc tgc ttt aag cag aag gct cgg   720
247 Leu Thr His Gly Pro Arg Thr His Ser Cys Phe Lys Gln Lys Ala Arg
248 225                 230                 235                 240
250 aga ctg act att ctg ctc ctc ctt gtt ttc tat ata tgt ttc tta ccc   768
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255 Phe His Ile Leu Arg Val Ile Arg Ile Glu Ser Arg Leu Leu Ser Ile
256                 260             265             270
258 agc tgc tcc atc gag agt cac atc cac gaa gct tac att gtt tct aga    864
259 Ser Cys Ser Ile Glu Ser His Ile His Glu Ala Tyr Ile Val Ser Arg
260         275             280             285
262 cca tta gct gct ctc aac acc ttt ggc aac ctg ctg tta tat gtt gtg    912
263 Pro Leu Ala Ala Leu Asn Thr Phe Gly Asn Leu Leu Leu Tyr Val Val
264     290             295             300
266 gtc agc aat aac ttc cag cag gca ttc tgc tct ata gtg aga tgc aaa    960
267 Val Ser Asn Asn Phe Gln Gln Ala Phe Cys Ser Ile Val Arg Cys Lys
268 305             310             315             320
270 gcc agt ggg gac ctt gaa caa gga aag aaa gac agt tgc tca aac aac    1008
271 Ala Ser Gly Asp Leu Glu Gln Gly Lys Lys Asp Ser Cys Ser Asn Asn
272             325             330             335
274 cct tga                                                            1014
275 Pro *
279 <210> SEQ ID NO: 4
280 <211> LENGTH: 337
281 <212> TYPE: PRT
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290         35              40              45
291 Pro Gly Asn Thr Val Ala Ile Ser Ile Tyr Ile Phe Lys Met Arg Pro
292     50              55              60
293 Trp Arg Gly Ser Thr Val Ile Met Leu Asn Leu Ala Leu Thr Asp Leu
294 65              70              75              80
295 Leu Tyr Leu Thr Ser Leu Pro Phe Leu Ile His Tyr Tyr Ala Ser Gly
296             85              90              95
297 Glu Asn Trp Ile Phe Gly Asp Phe Met Cys Lys Phe Ile Arg Phe Gly
298             100             105             110
299 Phe His Phe Asn Leu Tyr Ser Ser Ile Leu Phe Leu Thr Cys Phe Ser
300         115             120             125
301 Leu Phe Arg Tyr Val Val Ile Ile His Pro Met Ser Cys Phe Ser Ile
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303 Gln Lys Thr Arg Trp Ala Val Val Ala Cys Ala Gly Val Trp Val Ile
304 145             150             155             160
305 Ser Leu Val Ala Val Met Pro Met Thr Phe Leu Ile Thr Ser Thr Thr
306             165             170             175
307 Arg Thr Asn Arg Ser Ala Cys Leu Asp Leu Thr Ser Ser Asp Asp Leu
308             180             185             190
309 Thr Thr Ile Lys Trp Tyr Asn Leu Ile Leu Thr Ala Thr Thr Phe Cys
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VERIFICATION SUMMARY   DATE: 12/20/2005
PATENT APPLICATION: **US/10/529,278**   TIME: 10:29:12

Input Set : **A:\11582-010-999 Seqlist.txt**
Output Set: **N:\CRF4\12202005\J529278.raw**